2890

1115.

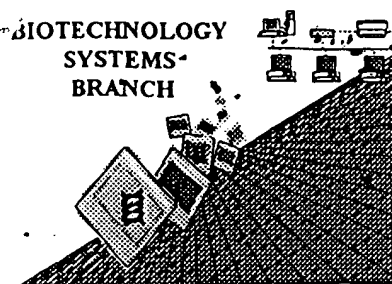# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/954456_   _#3_

Source: _OIPE_

Date Processed by STIC: _11/07/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/954,456

DATE: 11/07/2001
TIME: 15:21:39

Input Set : N:\EBONY'S\ES.txt
Output Set: N:\CRF3\11072001\I954456.raw

```
   3 <110> APPLICANT: Young, Paul
   5 <120> TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
Cancer Gene
   6       Sets
   8 <130> FILE REFERENCE: 689290-76
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/954,456
C--> 10 <141> CURRENT FILING DATE: 2001-09-18
  10 <150> PRIOR APPLICATION NUMBER: US/60/233,617
  11 <151> PRIOR FILING DATE: 2000-09-18
  13 <150> PRIOR APPLICATION NUMBER: US/60/234,052
  14 <151> PRIOR FILING DATE: 2000-09-20
  16 <150> PRIOR APPLICATION NUMBER: US/60/234,923
  17 <151> PRIOR FILING DATE: 2000-09-25
  19 <150> PRIOR APPLICATION NUMBER: US/60/235,134
  20 <151> PRIOR FILING DATE: 2000-09-25
  22 <150> PRIOR APPLICATION NUMBER: US/60/235,637
  23 <151> PRIOR FILING DATE: 2000-09-26
  25 <150> PRIOR APPLICATION NUMBER: US/60/235,638
  26 <151> PRIOR FILING DATE: 2000-09-26
  28 <150> PRIOR APPLICATION NUMBER: US/60/235,711
  29 <151> PRIOR FILING DATE: 2000-09-27
  31 <150> PRIOR APPLICATION NUMBER: US/60/235,720
  32 <151> PRIOR FILING DATE: 2000-09-27
  34 <150> PRIOR APPLICATION NUMBER: US/60/235,840
  35 <151> PRIOR FILING DATE: 2000-09-27
  37 <150> PRIOR APPLICATION NUMBER: US/60/235,863
  38 <151> PRIOR FILING DATE: 2000-09-27
  40 <160> NUMBER OF SEQ ID NOS: 2276
  42 <170> SOFTWARE: PatentIn version 3.0
  44 <210> SEQ ID NO: 1
  45 <211> LENGTH: 118
  46 <212> TYPE: DNA
  47 <213> ORGANISM: Homo sapiens
  49 <400> SEQUENCE: 1
  50 gaaaggtaca tatattcgtt tatgtctaaa ataacaacca gaatcttctt tatatatagt        60
  52 atttttaaaa gacacatata cacaaacaca aacatgtgca gtaaactcaa acacacaa         118
  55 <210> SEQ ID NO: 2
  56 <211> LENGTH: 427
  57 <212> TYPE: DNA
  58 <213> ORGANISM: Homo sapiens
  60 <220> FEATURE:
  61 <221> NAME/KEY: misc_feature
  62 <223> OTHER INFORMATION: n=a,t,g or c
  65 <400> SEQUENCE: 2
  66 atctaacaaa ggcactttat tgcattacca ttcacaatta acagtcaaga acaaataata        60
  68 ataacaaata aaataacttt taagaggaca aggcattaga aataaaaaag gacactaata       120
  70 acatttgtaa aagcttgtac tggatgtggt tgcccccatt tgtgtgtgtg gttgtgtgtg       180
  72 tgtggttgtg tgttggtggc cacagctgag cctctgtcac cagagaaggc tgaggcccaa       240
```

Does Not Comply
Corrected Diskette Needed

Errored must include location of unknown in field 222

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/954,456

DATE: 11/07/2001
TIME: 15:21:39

Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\11072001\I954456.raw**

```
W--> 74 tggcacacct cagaaaccta caccccgagg ctnggacggc tggactcctg agcacaagct     300
     76 ccctctcgca ccctttgcca gacagtttgt ctccaatttc aaactgacct aaggctctta     360
     78 ctcctggatt ttttgttttt aaaccttctc ccagccagtc ttcgggaggg catgattaga     420
W--> 80 gaagngg                                                               427
     83 <210> SEQ ID NO: 3
     84 <211> LENGTH: 412
     85 <212> TYPE: DNA
     86 <213> ORGANISM: Homo sapiens
     88 <220> FEATURE:
     89 <221> NAME/KEY: misc_feature
     90 <223> OTHER INFORMATION: n=a,t,g or c
     93 <400> SEQUENCE: 3
W--> 94 tttnnttttt tttttttttg tgtgtttttt tcttttaatg ccaagcacaa agtgtacatc     60
W--> 96 ataaaattca tatttggngt ttggcattat tttantaggt atgatcaaga ccacaaatat     120
     98 cttgccataa aaatattcta ctataataat gaaaaaatat atcattacat catcagtgac     180
    100 tcgaataaaa tatggtatag atatggcatt ttcaatgaaa gttggaagac acaccacatt     240
W--> 102 tgtactagtc ttaatatagg cacagtaaga agaacagata tttcccnctt tggctagtga     300
W--> 104 tatgcnttta gggtagttac gctgctgatt atcccagtga agttagtgtt gaggaaattc     360
W--> 106 tctttacttg ngccaaatct gcacttatgg gcaagactgt ggtacaagcn cc             412
    109 <210> SEQ ID NO: 4
    110 <211> LENGTH: 462
    111 <212> TYPE: DNA
    112 <213> ORGANISM: Homo sapiens
    114 <220> FEATURE:
    115 <221> NAME/KEY: misc_feature
    116 <223> OTHER INFORMATION: n=a,t,g or c
    119 <400> SEQUENCE: 4
    120 tgacagacca ggcttggcag tttatttcgg tttcacaacc cccttccagc ccttggggtc     60
W--> 122 ccttgagcag cacatctggg tgccctggcc ttcagcgggn agngngtcct ggggtcccag     120
W--> 124 cgcangangn gggagttccc ctttaggagt ctcactttcg gctgggcatt tctgggcttc     180
W--> 126 ctggggggca gatctggccg tgggggcaat ggaggagccn aaaggggcac ctgcccaggc     240
    128 tccaactccc tgccttcctg gtcactgctg ttccctgagt cctcagcagt agcctgaccg     300
    130 tagaactggt agatactcac ggcctcccag cccttgatct cgcagcggca gaaggggcag     360
W--> 132 gtctgggctg tccgagtgct gccaggcanc caggcagcag ctgcagaana ggtgcccgca     420
    134 cggctcaatc ttcacatcct tgttgctctc agcacagatc tt                        462
    137 <210> SEQ ID NO: 5
    138 <211> LENGTH: 261
    139 <212> TYPE: DNA
    140 <213> ORGANISM: Homo sapiens
    142 <400> SEQUENCE: 5
    143 gagggaaaga caaaacgtat ttattccagg ccaggtctta aaatgcacac tgcacggttc     60
    145 cctgttgtta tcagcaccag taaggaaaga acgtgcctta acggcagccc cacccagagc     120
    147 ctgctgcgtg gctgctgtga ggctccccat gaatccacgc agtcttcttc ctcactggtg     180
    149 cagttggtga ggttttctac cctcacagca aagggatcct taactataaa ttcacggtat     240
    151 gcagagaaga ggacagaatc t                                               261
    154 <210> SEQ ID NO: 6
    155 <211> LENGTH: 562
    156 <212> TYPE: DNA
    157 <213> ORGANISM: Homo sapiens
```

unknown must be enumerated in fields 221, 222 and 223. (handwritten annotation)

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors. (handwritten annotation)

file://C:\CRF3\Outhold\VsrI954456.htm

11/7/01

RAW SEQUENCE LISTING   DATE: 11/07/2001
PATENT APPLICATION: US/09/954,456   TIME: 15:21:39

Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\11072001\I954456.raw**

```
        159 <220> FEATURE:
        160 <221> NAME/KEY: misc_feature
        161 <223> OTHER INFORMATION: n=a,t,g or c
        164 <400> SEQUENCE: 6
        165 tagatttctc atagatttat ttctgcgtca tattatatat agatatatgc atatatacct      60
W-->    167 tttagcnaaa ggagancaat ctatataccc ttcccttccc caccaaactc acaaaaggag     120
W-->    169 attaaaccct tccaggattg ccatcaagct tcccgagatg gccagggcaa ngaaagaatc     180
        171 atctctcaac atgttaagaa acggctgcca ttcttaggct ctggggttga agcagcagca     240
        173 ttcccaggac ccaagggcca gagagaggaa aagaaatgac tgtagtgtga caggattcta     300
        175 ggatgaacat gtccagtgac tcctgggcat ggcagactag ctcccagaat tctcagggtg     360
        177 tgagtaaagg tgggggccct atggctcttc agaggctgct caataggtca ggggtagggt     420
        179 ataggaactg gggatcaggc atgcagggat ggggtggcag aaaaaacgcc tgtggggtta     480
W-->    181 tgctccagac agagcgaccc ccatcanggc tacccactac tcaatgacat gtaatgnaca     540
        183 gggacagatg ctgagctcct ta                                              562
        186 <210> SEQ ID NO: 7
        187 <211> LENGTH: 429
        188 <212> TYPE: DNA
        189 <213> ORGANISM: Homo sapiens
        191 <400> SEQUENCE: 7
        192 tggagataaa aacagcgaag tcccacatac cataccctac aagacacaag gtgcgcagac      60
        194 gagccttggt aatgtaccgg cgctgcagga agaggctgtc cgccgagcct gggctgctcc     120
        196 agctacgcgg ggaggcggcc ccattgcaaa gtgcagtttc tccgcggagg tggcggtggg     180
        198 tcagtggcag agggccatgg tttccatgtt aaggaagcgg acgtgcatct tggtctcaat     240
        200 gtcgatcccc tgccagatct tcaggaagtc ctcgaaggtg atcccctcgt acacctgatc     300
        202 aggctccatc ttgccccatg cacacgctgg ccgcctccat catggccccg tcggcgatgg     360
        204 agcgagcgga ctccttctcg atgtgagggt ttcccgacag cagctcctcg accactttac     420
        206 atttcgagg                                                             429
        209 <210> SEQ ID NO: 8
        210 <211> LENGTH: 348
        211 <212> TYPE: DNA
        212 <213> ORGANISM: Homo sapiens
        214 <220> FEATURE:
        215 <221> NAME/KEY: misc_feature
        216 <223> OTHER INFORMATION: n=a,t,g or c
        219 <400> SEQUENCE: 8
W-->    220 acataatccc tagtatagtc agatatattt atcacataga gcaactaggt tnaaatatag      60
        222 ttcagtgaca tttctagaga aactttttct actcccatag gctcttcaaa gcatggaact     120
        224 tttatacaac agaaatgttg acagaaattg ctgtagttta gggttgaagt actgtatgat     180
        226 gggcagcaat catgtattaa cttacgaagg ggaaattgaa atataggdac cgaatttggt     240
        228 tttatcagtt tccagagtac tgctgccaac ctagacactg attttttcaga gtttgaaatg     300
        230 taaatttctt cccgggactt tgattgcaca tgaagctgga ctgcgtta                  348
        233 <210> SEQ ID NO: 9
        234 <211> LENGTH: 652
        235 <212> TYPE: DNA
        236 <213> ORGANISM: Homo sapiens
        238 <220> FEATURE:
        239 <221> NAME/KEY: misc_feature
        240 <223> OTHER INFORMATION: n=a,t,g or c
        243 <400> SEQUENCE: 9
```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

```
         244 tgactttgct gatggtttat taccttaagg aaaagactta cacagagaaa ttgagcaatg      60
         246 aaaacccttc acattgagca aacacattcc acgctacaca aatcatgaga aaaatgagaa     120
         248 ctgttgtgaa acatgacaga ttgcccaagt gttatttttc ctctattgga aaattctaag     180
         250 acgtttcctc atgtgtagtt tttcagtcac aaaaatggca gtaggaatat ttaaatatta     240
         252 aatcacagtt tgaaaataga tacatacata catatatata cacacacaga gatacatagt     300
         254 tgacttatga ttcccagata tgcagggtta tcattgtgac tgcttggatc aagacaagtt     360
         256 tgtaaaaagc agcgacatag ttcaacataa tagtcaggag ctagattact tccctgtaat     420
         258 tgctatgcac acacagtaca aggctagcga gattatagac aatctgtctt cgaatctact     480
         260 atcttgataa ttctgaatct tttcaagtta aaattgcagc tattgtcagt aagcgcccct     540
W--> 262 ataaaggtca ggcctttgan tgggggacga taactngcgt caccaggaga gaggcncggt     600
W--> 264 tcaacttccn ggttccgtct ggcngcggtc acagccggna acctgggtcc cg             652
         267 <210> SEQ ID NO: 10
         268 <211> LENGTH: 614
         269 <212> TYPE: DNA
         270 <213> ORGANISM: Homo sapiens
         272 <220> FEATURE:
         273 <221> NAME/KEY: misc_feature
         274 <223> OTHER INFORMATION: n=a,t,g or c
         277 <400> SEQUENCE: 10
W--> 278 nggctgtgat aggtttattc agaggaagca ctagactctg gggtagctca catgggtaag      60
         280 aaagacttcc aggagcaggc attgaagggt tggcaccctg ggtgagtgtc caaggtcagc     120
         282 gagagtcact tgtggagggg acggaagatg acctggctga tctggccagg gatggtgtag     180
W--> 284 aagaccagga ggaggaagac ggtgagcagc accagtagca gcagcaccag ggtngcccag     240
W--> 286 taccggcnca gatgaagaag acaaaggcct tcagcgggtt cacaaaccag ttgaaggaag     300
         288 ttttggggcg gctgggtttc tccagaaggc tcttggctgc ttccgcccct tccccattgg     360
W--> 290 ccgtttctcg ggcttccttc cacagtcaag caagctcaaa ctcttgcctc caacnttgcc     420
W--> 292 cgtgaagaat gtacacattg gcanccatgt ctgtgaactc ccangtcttt ttggccggcc     480
W--> 294 ttcctcctcc tctgctttcg cttcttcttg caagcctgag cctcctgngc ttccggtcaa     540
W--> 296 gtccttgctc cttaagttna ataacggcaa cagccctcaa gggggaaga aacagattga     600
W--> 298 ctcngccggc ccat                                                       614
         301 <210> SEQ ID NO: 11
         302 <211> LENGTH: 187
         303 <212> TYPE: DNA
         304 <213> ORGANISM: Homo sapiens
         306 <400> SEQUENCE: 11
         307 tttttgagac atgaaaacgt atgcattttt attaaccaga tttttaaaaa aggacaaagg      60
         309 cacatgtatc agggtgccgg gggtgcatgg tgtacatctg atttcataag caatgtcagt     120
         311 ctcctctaaa ctggcatcct gcgcttgaca ggtaggcaga acaaacggga cgctggcacc     180
         313 ggaacct                                                              187
         316 <210> SEQ ID NO: 12
         317 <211> LENGTH: 349
         318 <212> TYPE: DNA
         319 <213> ORGANISM: Homo sapiens
         321 <400> SEQUENCE: 12
         322 tttctcggtc aataatttat tagtaaaata tacatttctc attattaaag aataaaagct      60
         324 ttcagccctg ctgaacacac atctgaggtc tcaagaaaac cagacaagat agctgactct     120
         326 cccacatagc cctttccata aaggcgattc ctaagcttaa acacacacaa agctggggct     180
         328 gtccctcttg aatcccatgg gaaacaggcc ccaagatcag gggacctgga gtcgggagct     240
         330 tggggtgcag tctgctcact gacaccctct cgaagagcac gcaggggaac ctggtcctgg     300
```

RAW SEQUENCE LISTING   DATE: 11/07/2001
PATENT APPLICATION: US/09/954,456   TIME: 15:21:40

Input Set : N:\EBONY'S\ES.txt
Output Set: N:\CRF3\11072001\I954456.raw

```
332 gatggagtct ttctggggat gcccacgtct gtgctgcctg gaaccgggt          349
335 <210> SEQ ID NO: 13
336 <211> LENGTH: 476
337 <212> TYPE: DNA
338 <213> ORGANISM: Homo sapiens
340 <400> SEQUENCE: 13
341 tcacatttgt atgtgtcatt tatttcggtt gcgctgggga aagagaacgc agtttctctc    60
343 cccgcctcct cctcgctggg tagaactaac tctaaaacac caatatctca acactgaacc   120
345 ctcccaaatc gcaagagttt tcttttcccc ttccttgttt ttcttttaa gctgattggc   180
347 ttttgtctat cttgctcttt cctttttcttt ttcgtctctc ccccgcctgt gttggggtat   240
349 tttgtggggt ttttgttttt cccctggctg tgctgaggca gcaggctggg tagggtttag   300
351 gactgctcct tgtcggtttt ctctttattc atcttttttca tcttcatcct tcgattctga   360
353 aaccagattt tgacctgccg ctcggtgaga ttgagaaccc gggccacctc ataccgacgg   420
355 tccctggtta aatacatatt gaagagaaac tccttctcca gttccagcgt caggta        476
358 <210> SEQ ID NO: 14
359 <211> LENGTH: 388
360 <212> TYPE: DNA
361 <213> ORGANISM: Homo sapiens
363 <400> SEQUENCE: 14
364 tgggggtagg ctctttatta gacggttatt gctgtactac agggtcagag tgcagtgtaa    60
366 gcagtgtcag aggcccgcgt tcagcccaag aatgtgggat ttctctccct attgatcaca   120
368 gtgggtgggt ttcttcagaa aagccccaga ggcagggacc agtgagctcc aaggttagaa   180
370 gttggactgg aaggcttcag tcacatgctg ctttcaagct ttcaggctgg gcaacaagga   240
372 ggagatgccc atgacgtgcc agggtctccc catctgacac cagtgaagtc tggtaagaca   300
374 gcagccgcac gcctgcctct gccaggaggg caatcatggt aggcagcatt gcagggtcag   360
376 aggtctgagt ccggaatagg agcaaggg                                     388
379 <210> SEQ ID NO: 15
380 <211> LENGTH: 461
381 <212> TYPE: DNA
382 <213> ORGANISM: Homo sapiens
384 <400> SEQUENCE: 15
385 tgcggccgcc tccatgaagc ggaaaagcga gccgcggtcg agctgggccg ccgcccccccc    60
387 tgctcgcggg ctgctcgtcg acctcgccgg gtgtgaagaa gatccgcagc tccacgcagc   120
389 aagacccgcg ccgccggacc ccccaggacg acgtgtacct ggacatcacc gatcgccttt   180
391 gttttgccat tctctacagc agaccaaaga gtgcatcaaa tgtacattat ttcagcatag   240
393 ataatgaact tgaatatgag aacttctacg cagattttgg accactcaat ctggcaatgg   300
395 tttacagata ttgttgcaag atcaataaga aattaaagtc cattacaatg ttaaggaaga   360
397 aaattgttca ttttactggc tctgatcaga gaaaacaagc aaatgctgcc ttccttgttg   420
399 gatgctacat ggttatatat ttggggagaa ccccgaagaa g                      461
402 <210> SEQ ID NO: 16
403 <211> LENGTH: 339
404 <212> TYPE: DNA
405 <213> ORGANISM: Homo sapiens
407 <400> SEQUENCE: 16
408 aaggagggat gtctgtttat ttacagtgca ccctttgtgc caggccctta tgttcatgac    60
410 cttacccaac tctacaatct tgcaaggcgg tttacatcat ctccacttta cagttcaaga   120
412 aacaaaggct cagattcata gcccctgaat agtccctcat agtccctgag ttcataagta   180
414 gtggttatag tacaatctaa gctatttaat tccaaagcca gtgatttttc tggccttgag   240
416 ctataggtcc aaaggctcca acagggccct ccagactcaa tggcagggtg gtgtctgcac   300
```

VERIFICATION SUMMARY   DATE: 11/07/2001
PATENT APPLICATION: US/09/954,456   TIME: 15:21:41

Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\11072001\I954456.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Current Application No
L:10  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:74  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:74  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:80  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:80  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:94  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:94  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:96  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:96  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:102 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:104 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:122 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:124 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:167 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:169 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:181 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:220 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:262 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:278 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:284 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:286 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:290 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:292 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:294 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
```

VERIFICATION SUMMARY   DATE: 11/07/2001
PATENT APPLICATION: **US/09/954,456**   TIME: 15:21:41

Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\11072001\I954456.raw**

```
L:296  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:296  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:298  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:298  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:867  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:867  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:955  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:41
L:955  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:2619 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2621 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2637 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:2637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:2643 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:2643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:2645 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:2645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:2663 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2667 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2669 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2671 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2673 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2689 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:2689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2697 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:2697 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2699 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:2699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2701 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:2701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2719 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:2719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:2721 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:2721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:3163 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:55
L:3163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:3717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:60
L:3717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:3768 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:62
L:3768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:3842 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
L:3842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:3860 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
```

VERIFICATION SUMMARY　　　　　　　　　　DATE: 11/07/2001
PATENT APPLICATION: **US/09/954,456**　　　TIME: 15:21:41

Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\11072001\I954456.raw**

```
L:3860 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:3862 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
L:3862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:3864 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
L:3864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
```

ERROR DETECTED	**SUGGESTED CORRECTION**	**SERIAL NUMBER:** 09/954456

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1. ____ Wrapped Nucleics
   Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2. ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3. ____ Misaligned Amino
   Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4. ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5. ____ Variable Length.

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6. ____ PatentIn 2.0
   "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7. ____ Skipped Sequences
   (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8. ____ Skipped Sequences
   (NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9. ____ Use of n's or Xaa's
   (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10. ____ Invalid <213>
    Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11. ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12. ____ PatentIn 2.0
    "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13. ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MII – Biotechnology Systems Branch – 08/21/2001